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INTEGRATED INFORMATION SYSTEM FOR MULTI-CRITERIA MANAGEMENT OF ORTHOPEDIC INFECTIONS

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Abstract

The detection of an infection with or without the presence of prosthesis (mainly hip and knee) remains today very delicate. Primarily, the difficulty of differential diagnosis between mechanical loosening and septic loosening of prosthesis comes from the torpid nature of chronic infections. Secondly, as the diagnosis of orthopedic infections is a multidisciplinary approach that generally lasts for months (not to say years for complex cases), it tends to generate a huge amount of heterogeneous data that is scattered in the hospital environment. Inadequate or late diagnosis as well as inadequate treatment (such as unsuitable antibiotherapy) due to poor initial diagnosis may be the cause of disabling pain, lasting damage and complications for the patient, not to mention the significant direct and indirect costs to the patient and society. In this paper, we present a complete platform for the diagnosis of osteoarticular prosthesis infections, incorporating innovative modules from both imaging processes and molecular biology processes, an intelligent data management system including multidisciplinary, mobile and adaptive user interfaces, while ensuring full traceability of diagnosis.

Keywords

Infection orthopedic, Information System, Molecular Biology, Ontologies.

Introduction

The diagnosis of orthopedic infections [12] is a tedious, long, expensive and complex process. Its complexity is that many infections can take several months to develop. In the case of acute infections, a rapid response is required to contain the disease. However, early antibiotic response not suitable can generate to resistant bacteria. Imaging, given the similarity of observed features in the case of skeptics and septic loosening, an overlap with the patient's history and local punctures are required for proper discrimination. The diagnosis of orthopedic infections requires multidisciplinary approach [10], such as, the molecular biology, orthopedics, radiology, and nuclear medicine. However, at present, there are not IT tools that integrate these different disciplines and there are not comprehensive guidelines to optimize the detection and management treatment of the patient. The detection of an infection is the first step. Indeed, in order to allow an effective therapy, it should be able to identify the causative agent of the disease. Conventional culture methods [16] have drawbacks that may hinder the identification process. Firstly, some bacteria are known to have a slow growth, which can range from several days to several weeks, a period which may establish a risk to the infected patient. Secondly, the handling of live bacteria induces a significant risk of contamination. Finally, the specificity of the culture technique is not always sufficient because many results turn out to be false negatives. Therefore, the cost related to the process of developing the infection diagnosis is a result of many hospitalizations and repeated imaging tests.

Imaging serves a lot in the elaboration of the diagnosis by the implementation of different mechanisms of detection of observable lesions coming through the pictures from different (morphological and functional) imaging modalities. This detection requires the image enhancement via filtering techniques and segmentation, but also by the fusion of multimodal images, thus taking advantage of the various existing methods.

Like imaging, we use a specific gene amplification technique called PCR (Polymerase Chain Reaction). PCR is used to extract information about the presence and identification of bacteria potentially responsible for disabling pain in the patient. Genetic kit aims to develop a molecular method for rapid and unambiguous identification of infectious agents in orthopedic pattern.

In this paper we present the model and the architecture of a collaborative platform to help in the data integration between clinical, imaging and laboratory exams in the context of orthopedic.

Analysis

A Decision Problem

Determining a diagnosis (or a therapeutic solution) is about making a decision: a set of features [6] (clinical

symptoms, imaging observations, patient anamnesis, etc.) is observed, patterns are extracted and associated with a disease. Typically, to handle such decision problem, we resort to a mathematical formalization where each disease is defined as a class or model, which details its functional or descriptive properties. Thanks to such a representation, it is possible to reason on data and make the adapted classification.

The decision process can be structured into three steps [3]: the identification and the structuration of the decisional problem and the making of a choice.

The identification of the problem is intended to mark out the perimeter of the domain and define a relevant scope. In a medical context, taking every bit of information will be likely to induce a form of noise for the reasoning. It is important to filter out the data and focus on the most discriminating features. As far as that goes, the level of abstraction for the modeling helps to reduce the complexity of domain. Thus, the better the focus filter and the level of abstraction are, the better will be the classifications.

The structuration of the decisional problem refers to the definition of diagnosis hypothesis. Usually, those rules are setup with the help of experts of the domain so the inferences will correspond to the real-world interpretations.

The last step of choosing the solution is about substituting the rules from step two with the filtered data from step one. Typically, this step also refers to learn knowledge from previous inferences: anterior decisions will influence current decisions.

The next two parts highlight the difficulties in structuring medical data, rules and making inferences since the interpretations in the real-world are not Manichean.

A Medical Context

Elaborating a diagnosis, especially in the domain of orthopedic infections, requires a multidisciplinary study of the case that can take months, not to say years (for chronic infections) [11]. Generally, this process tends to generate a huge amount of heterogeneous data scattered in the clinical environment. Moreover, these data are associated with a complex and technical vocabulary thanks to which doctors communicate. In such a context, it is essential to rely on a model with the right abstraction level and favor communication channels in order to ensure the cooperation between the members of the medical staff. This aims to manage the data in an adapted and optimal way. “Adapted” means to be able to focus on a particular set of data from various disciplines and that are relevant for the current suspected pathology. It also refers to data presentations adapted to the domains of expertise. “Optimal” is about the formalization of data exchange and the assurance of complete traceability of relevant diagnosis information used in the inferences.

For the circulation of data among the interconnected systems, the medical community has developed communication and data formatting standards such as DICOM or HL7 [8][4][7]. It is crucial to rely as much as possible on such standards to limit the fragmentation and redundancy of data and facilitate the data centralization, comparison and the pattern (associated to a particular disease) matching. In addition, it will serve the portability and re-usability of the system. Also, knowing the growing demand for the use of mobile devices, it is important to provide systems with interoperability capabilities with smartphones and tablets.

Reasoning and uncertainty

In order to model the real-world knowledge about a medical domain, we need to consider uncertainty. For instance, how to represent the uncertain relations between bacteria and antibiotics in statements such as “Mycobacterium Smegmatis is resistant to Rifampicin with a probability greater than 90%”?

Uncertainty in medical knowledge is represented with probabilistic models [2], which are considered as the scientific norm for this purpose. Often, Bayesian Networks [13] are used to formalize the probabilistic link existing between concepts from the medical domain. However, this requires providing the knowledge base with an a priori acyclic graph linking the entities. Such a construction can be difficult in a medical context. Moreover, working with acyclic oriented graphs prevents from modeling some complex relations between data in order to take advantage of the probabilistic information in both ways: from entity A to entity B and backwards.

Method

Abstraction Layer Approach

The approach used to fulfill the objectives present in the implementation of the platform is presented in Fig. 1 as an abstraction layers model. This approach allows dividing the complexity of the system into several levels. Each level is designed a part of the system and make workable outputs for the higher layer. Fig. 1 presents the data transformation (bottom-up) up to the diagnosis. The lowest layer represents the hospital environment with different information sources. It is composed mainly of imaging systems, medical records, electronic patient record and information resulting from laboratory tests. The first level of the platform is for the standard connectors. These can interact with entities in the hospital and provide the necessary means of communication to the flow of information (from the hospital to platform and vice versa). The top layer is based on the functionalities offered by the lowers layer to extract the data relating to the patient and used for

diagnosis. These data are formalized and transformed into variables of the system. This task is performed by the semantic annotation layer and sends to the inference layer. The data must be logically structured to allow a machine to interpret the information and make diagnostic inferences. Finally, a processing data layer adapts the information presentation in the visualization context.

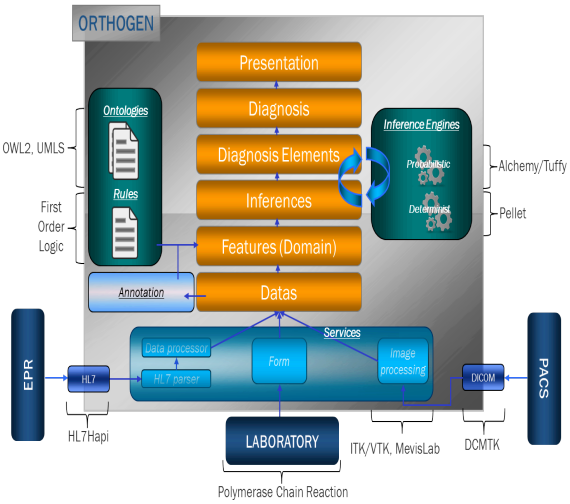

Fig. 1: Scheme Manager Model

Due to the implementation of the image extraction algorithms and genetics kit, new information elements may be associated with the patient symptoms. These data are quite diverse and without a precise semantic structure. To enable a machine to reason about these data, we must assign them to a precise semantics and associate them with clear and unambiguous concepts. These concepts are classified according to a precise taxonomy and established relations to define the domain of the medicine, which you plan to work (bone and joint infections). This combination of words to concepts of a domain is the annotation. For the different types of annotation (structural, linguistic, semantic), we formally define the domain of hip prosthesis infection. The chosen approach is to use an ontology [1] that will allow us to establish taxonomy of concepts, relate, instantiate and make inferences [1]. We have developed a specific medical ontology for the domain of orthopedic infections. The ontology developed was done in collaboration both with medical experts and with the standard UMLS [15] to ensure a level of quality during the inference.

Markov Logic

Traditionally, the probabilistic information is integrated at the ontology level. Some approaches provide an ontology model to classify the probabilistic information (such as PR-OWL [9]). Knowing the difficulty modeling a medical domain can be, overloading the model with probabilistic entities might lead to a complicated representation harder to maintain. Another approach is to extend the ontology and give primitives to represent the probabilistic information. Ex: Pronto [9] which extends the traditional DL's [1] in a way that allow associating a probability value to the axioms. The shortcoming of such an approach is the backward compatibility with existing inference engines. Indeed, a specific engine has been developed to be able to reason on data according to the new syntax and semantic.

Our approach the probabilistic information is outside the ontology at the first order logic level [1] and relies on the Markov logic [5]. The advantages are: compatibility with OWL2 [11] (DL and rules), Markov Logic inputs and earnings opportunities offered by the probabilistic inference algorithms [6].

Results

The architecture was implemented with aims the developing the generalization capabilities and reusability of the platform for the domains (medical) and environments (hospital and software) different. In addition, with the current trend towards decentralization and mobility of the supports, we have focused in the programming client/server paradigm. This allows to make the platform compatible with all types of customers, whether heavy (implemented in Java, C++, etc.) or as a directly accessible Web site from any browser. Beyond compatibility, knowing that heavy processing (deterministic and probabilistic inference, image processing, etc.) are supported on the server-side, client machines should not have prohibitive hardware configurations: a smartphone or tablet allows control of the platform.

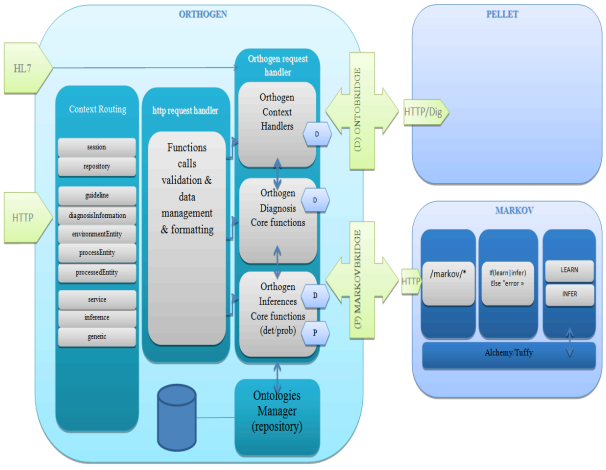

Fig 2: Information System Architecture.

Fig. 2 shows the platform components and technologies used. The modules for the management of data and logical inferences are decoupled to keep a certain modularity to work with multiple engines. In our case, we have used Pellet [11] to ensure

deterministic inferences and remote interactions are performed using the DIG interface. For probabilistic inference, we developed a specific engine accessible from the web and relying on Tuffy framework [14] whose management approach is based on probabilities Markov logic [5]. The implementation of platform is divided into three layers:

1) A first layer is defined as an API, which can interact with the remote server.
2) A second layer intercepts the calls to the methods and supports the management of requests.
3) The third layer includes all handlers called from the layer level two and they will perform the data managing tasks.

Fig. 3 show the GUI of a Java client connected to the platform and to manipulate the contents of a diagnosis. The left part shows instances medical concepts and the right side the data descriptors associated with them. Accordance with the desired goal of generalization and reusability of the platform, managing information about a diagnosis is generic.

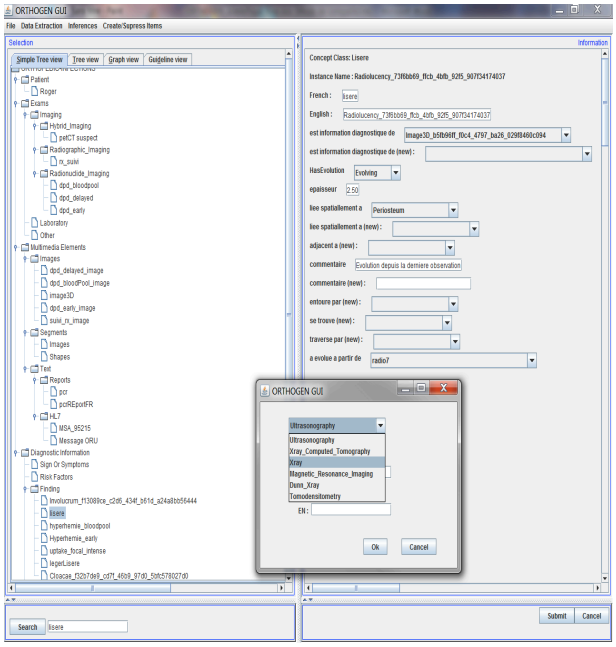

Fig 3: GUI Java client connected to the platform.

Conclusion

The platform that we have implemented is based on a model of data management in abstraction layers, which is capable of receive several medical domains and modeling them using a meta-model diagnosis defined. On this basis, it is possible to handle medical information, perform operations on the media produced by imaging modalities, but also to extract data from reports generated by laboratory or messages obtained after exchanges with the medical record computerized. As the platform is capable to model several domains using a meta-model diagnosis defined, these meta-models working at a certain data abstraction level, they are independent of a specific representation and can be represented in various forms. As essential management and inferences data are performed of the server side, the platform can be accessed remotely via the HTTP protocol, modeling using the Representational State Transfer architecture, any mobile device capable of making HTTP requests can interact with platform, regardless of technical limitations (CPU, main memory or storage, etc.) or ergonomic (screen size, limited devices etc.). Finally, the processes around of the platform are the mobility dimension, server modeling according to the principles of service-oriented architecture, diagnostic guidelines modeling, the integration of a probabilistic inference engine based on Markov logic (classical vs. Bayesian approach).

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